

FIG. 1A

(SEQ ID NO:1)

5' GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT

 ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA

 (SEQ ID NO:2) M E S R K D I T N Q E E L W K

 ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA

 M K P R R N L E E D D Y L / H K D T G

 GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CA ACA GCC CAT

 E T S M L K R P V L L H L H Q T A H

 GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA

 A D E F D C P S E L Q H T Q E L F P

 CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT

 Q W H L P I K I A A I T A S L T F L

 TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT

 Y T L L R E V I H P L A T S H Q Q Y

 TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC

 F Y K I P I L V N K V L P M V S I

 ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT

 T L L A L V Y L P G V I A A I V Q L

 CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA

 H N G T K Y K K F P H W L D K W M L

 ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT

 T R K O F G L L S F F A (V) L H A I

 TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG

 X S L S X P M R R S Y R Y K L L N W

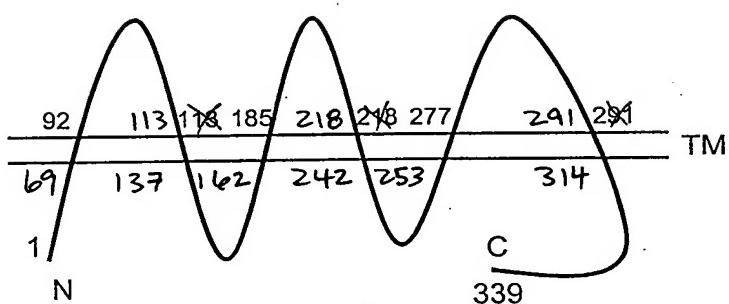
 184 185

.....100010667.040402

659 660 670 686 695 704
GCA TAT CAA CAG GTC CAA CAA AAT AAA GAA GAT GCC TGG ATT GAG CAT GAT GTT
A Y Q Q V Q Q N K E D A W I E H D V
713 722 731 740 749 758
TGG AGA ATG GAG ATT TAT GTG TCT CTG GGA ATT GTG GGA TTG GCA ATA CTG GCT
W R M E I Y V S L G I V G L A I L A
767 776 785 794 803 812
CTG TTG GCT GTG ACA TCT ATT CCA TCT GTG AGT GAC TCT TTG ACA TGG AGA GAA
L L A V T S I P S V S D S L T W R E
821 830 839 848 857 866
TTT CAC TAT ATT CAG AGC AAG CTA GGA ATT GTT TCC CTT CTA CTG GGC ACA ATA
F H Y I Q S K L G I V S L L L G T I
875 884 893 892 891 890
CAC GCA TTG ATT TTT GCC TGG AAT AAG TGG ATA GAT ATA AAA CAA TTT GTA TGG
H A L I F A W N K W I D I K Q F V W
909 918 947 936 935 974
TAT ACA CCT CCA ACT TTT ATG ATA GCT GTT TTC CTT CCA ATT GTT GTC CTG ATA
Y T P P T F M I A V F L P I V V L I
923 922 1001 1010 1019 1028
TTT AAA AGC ATA CTA TTC CTG CCA TGC TTG AGG AAG AAG ATA CTG AAG ATT AGA
F K S I L F L P C L R K K I L K I R
1037 1046 1055 1064 1073 1082
CAT GGT TGG GAA GAC GTC ACC AAA ATT AAC AAA ACT GAG ATA TGT TCC CAG TTG
H G W E D V T K I N K T E I C S Q L
1091 1100 1109 1118 1127 1136
TAG AAT TAC TGT TTA CAC ACA TTT TTG TTC AAT ATT GAT ATA TTT TAT CAC CAA
* N Y C L H T F L F N I D I F Y H Q
1145 1154 1163 1172 1181 1190
CAT TTC AAG TTT GTA TTT GTT AAT AAA ATG ATT ATT CAA GGA AAA AAA AAA AAA
H F K F V F V N K M I I Q G K K K K
AAA AA 3'
K

FIG. 1B

Extracellular



Intracellular

FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3' (SEQ ID NO: 3)

FIG. 4 - 1

GGGGCCCGCACCTCTGGGCAGCAGCGCAGCCGAGACTCACGGTCAAGCTAAGCGAAGAGTGGTGGCTGAAGCC
ATACTATTTATAGAATTAA~~TG~~GAAGCAGAAAAGACATCACAAACCAAGAAGAACCTTGAAATGAAGCCTAGG
AGAAAATTTAGAAGAAGACGATTTCGATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTGC
ATTCGACCAAAACAGCCCATGCTGATGAATTGACTGCCCTCAGAACCTCAGCACACAGGAACCTTCCACAA
GTGGCACTTGCACATTAAAGCTGCTATTAGCATCTGACTTTCTTACACTCTCTGAGGGAAAGTAATT
CACCCCTTAGCAACTTCCCACATCAACAATATTTTATAAAATCCAACTCTGGTCACTCAACAAAGTCTGCCAATGG
TTTCCATCACTCTTGGCATGGTTACCTGCCAGGTGTAGCAGCAATTGCTAACATGCTAAATGGAACCAA
GTATAAGAAGTTCCACATTGGTGGATAAGTGGATGTTAACARGAAGCAGTTGGGCTCTGAGTTCTT
GCTGACTGCATGCAATTATAGTCTGCTTACCCAAATGAGGCATCCTACAGATAACAGTTGCTAAACTGGCATT
ATCAACAGGTCAACAAAATAGAAGATGCCGGATTGAGCATGATGTTGGAGAATGGAGATTATGTTCT
GGATTGTGGATTGGCAACTGGCTCTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTGACATGG
AGAGAATTTCACATATTCA~~GAGT~~AAATAATATAAAACCTAACAGGTAATCTTCTTTGTGTTATGAT
ATAGAATATGTTGACTTTACCCATAAAAATAACAAATGTTTCAACAGCAAAGATCTTACATTGCTTCAATT
ATAATGTGCTCCTCTGGTTTCCATTGCTTCAATTAGGACAAGTGTCTAGACATAAAATAAGGCAT
TAAATATTCTTGTGTTTTTTGTTGTTGTTGTTGTTGTTGTTGAGATGAAGTCTCG
CTCTGTTGCCATGCTGGAGTACAGTGGCACGATCTGGCTCACTGCAACCTGCGCCTCTGGGTCAGGCATT
CTCTGCTCAGCCTCTGAGTAGCTGGATTACAGGCACCCATCACCAGTCCAGCTAAATTGTTGTTGTTGAGATGAAGTCTCG
GAGACAGGGTTTCCATGTTGCCAGGCTGGCTCGATCTCTGACCTCAAATGATCCGCCACCTGGCCTCCC
AAAGTGGGATGACAGTTGAGGCCACACTCAGCTGCTTTCTAAATTGAAACTTGTAGACAATT
GCTACCCATCTAATGTGATATTAGGAATCCAATATGCTAGGTTATTATCTTAAAAAATATTCTTAC
TGTCTACCTGAAGTTCTAAATATTCTGTAATTAAAATCTCAGATTACTGAGGTTATCTTCTGGT
GGTAGATTATCCATAAGAAGAGTGTGCCAGAACACTCTGGATCTGTGACAAGATTCAAAGGACTAA
TTAATTCACTGAAACACTGCCATTACCGTTATGGTAGACATCTTGGAAATTCCACAAGGTCAAGACATT
GCCAACTATCCCTCTACATGTCCACACGTATACTCCAAACACTTTATTAGGCATCTGATTAGTTGGAAAGTATGC
CTCCATCTGAAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTCTAAATTGTTAGGTCAG
CCTGATAACCACTGGAGTTCTTGGCTCTTAAATAGCTTCTCACACATTGCTGCCCTGTTACACATATGA
TGAACACTGCTTTAGACTCATTAGGAATTAGGACTGCATCTGACAACGTGAGCCTATTCTACTATATGTACA

FIG. 4-2

ATACCTAGCCCATAATAGGTATACAATACACATTGGTAAACTAATTTCAACCAATGACATGTATTTCAACT
AGTAACCTAGAAATGTTCACTTAAATCTGAGAACCTGGTACACTACAAGTACCTTGAGATTCATATATGAAA
ACGCAAACCTAGCTATTGATTGATTCACTGGACTTAAGAATGCCCTGAATAATTGTGAGTCGATTGTTCT
GGCAGGCTAATGACCATTCCAGTAAAGTGAATAGAGGTAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT
TGAGATTACATAGGTGAACAACTATTAAAGCAACTTTATTGTGTTAGTGCAGACATTGAAAAAATTGTTCAATTATTCCATGTTAC
ATGTTCATCACATCTCTGGATCTCTATTGTGCGAGACATTGAAAAAATTGTTCAATTATTCCATGTTAC
AGAATATTGATTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCAATTCAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACGTATAAGATCACTGAAGTCAAATTGATTTTGCTATAATCTCAATCTACCTATAT
TTAATTGAGAATCTAAATGTACAAATCATTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT
GATTTAGGTATCCTGTGAAAGCAGAATTAAAGACAAACACAAGAGACAAAGCACAACAAATAATCATAAAG
GGGATGAACAAATGGTGGAGAAAGAGTAGACAAAGTTTGATCACCTGCCCTCAAAGAAAAGGCTGTGAATTG
TTCACCTAGACAGCTGGAGACAAGAAATTACCCAAAGTAAGGTGAGGAGGATAGGCAAAAGAGCAGAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAACAAATCATAGATAAAGGATTCCAAGAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAACTCTTATTGAACCAATCTCACCATTGTTTCTCTGCAGAGCTAGGA
ATTGTTCCCTCTACTGGGACAATACACGGATTGATTTGCCCTGGAATAAGGTAGATATAAAACAAATTG
TATGGTATACACCTCCAACCTTATGATAGCTGTTCTCCAATTGTTGCTGTATTTAAAGCATACTATT
CTGCCATGCTGAGGAAGAAGATACTGAAGATTAGACATGGTGGAGACGTCACCAAAATTAAACAAACTGAG
ATATGTTCCAGTGTAGAATTACTGTTACACACATTGTTCAATTGATATTATTCACCAACATTCA
AGTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAA (SEQ ID NO:6)

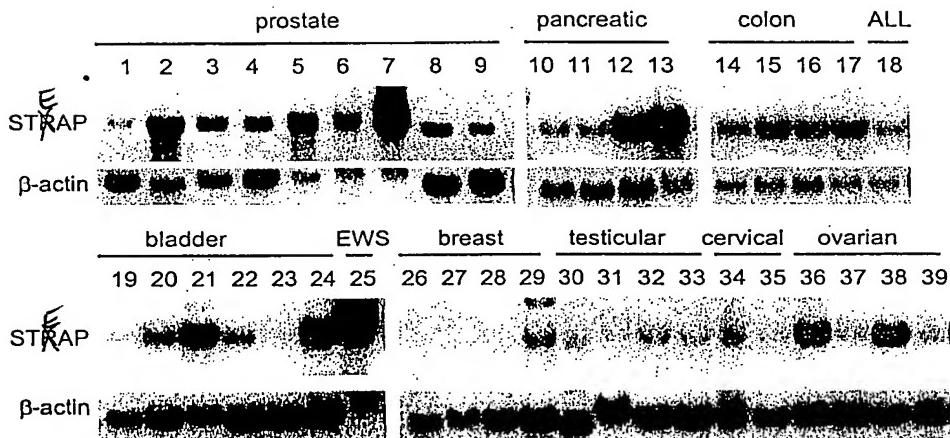
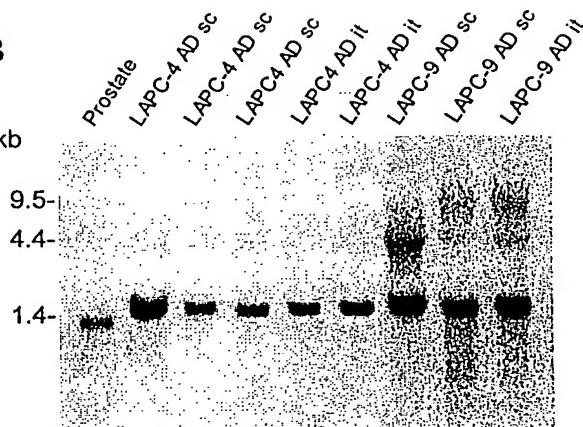
FIG. 5**A****B**

FIG. 6

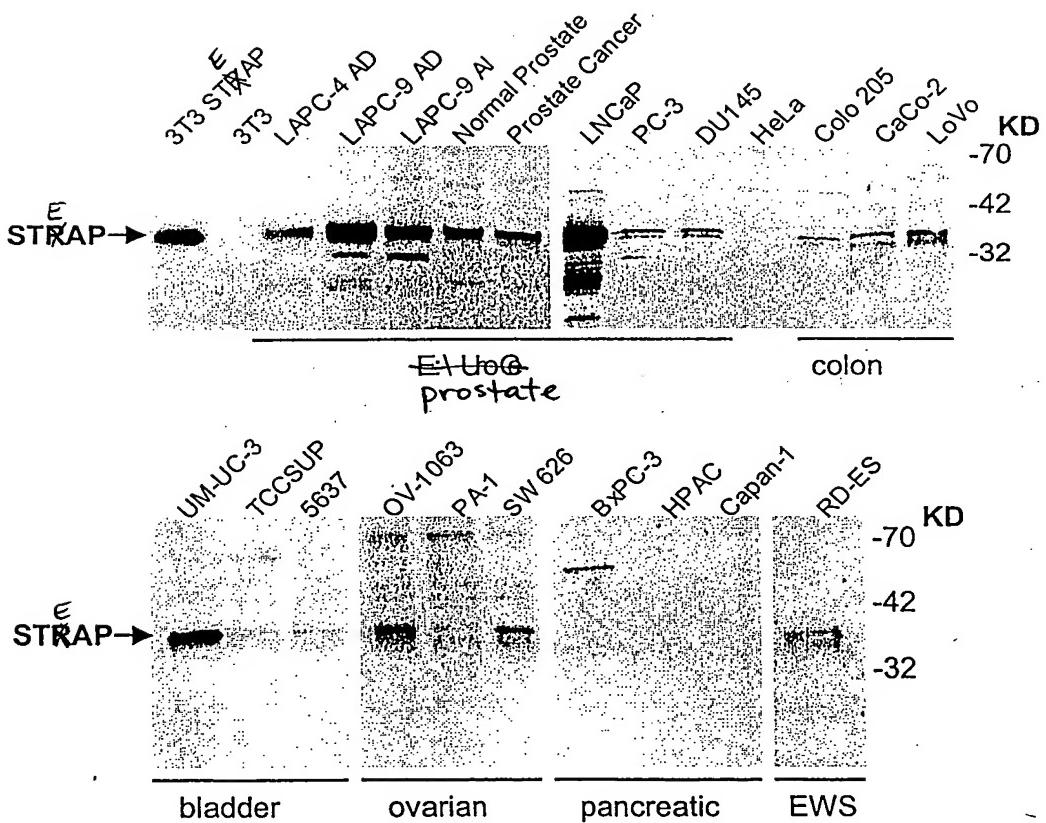


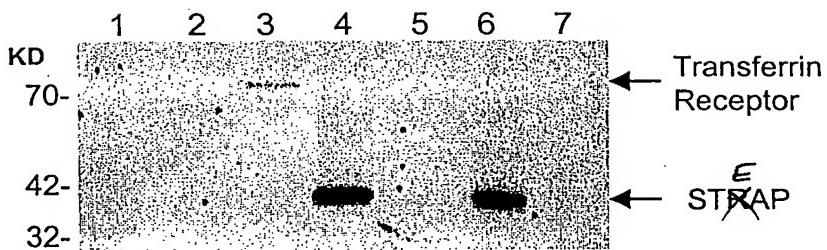
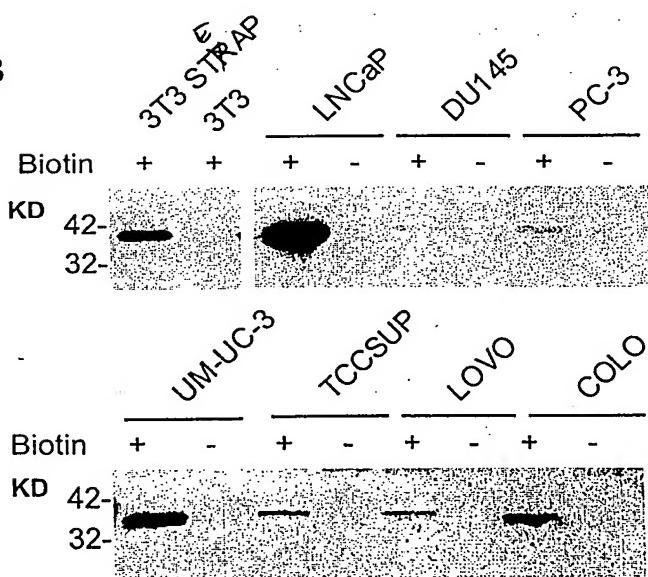
FIG. 7**A****B**

FIG. 9

10 19 28 37 46 55
 5' GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC

 Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

 64 73 82 91 100 109
 ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA

 Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

 118 127 136 145 154 163
 CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA

 Leu Tyr Tyr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

 172 181 190 199 208 217
 CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC GCT ATG GTC CAT GTT

 Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

 226 235 244 253 262 271
 GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC

 Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

 280 289 298 307 316 325
 ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA

 Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

 334 343 352 361 370 379
 GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT

 Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

 388 397 406 415 424 433
 TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA

 Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

 442 451 460 469 478 487
 GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT

 Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

 496 505 514
 TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3' (SEQ ID NO:7)

 Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala (SEQ ID NO:8)

FIG. 10

STAP-2, AA508880 (NCI_CGAP Pr6)

ggtcgactttcccttattcccttgtagagatctgattcatccatatgtcttagaaaccaacagagtgactttaca
aaattccatagagattgtgataaaaaccttatctatgtgcattacttgcctccctatgtataccctgcagg
tcttcgtcgactgtcttatcaatttacggcacaaggatagaggatccatgtggaaacctggta
cagtgttagaaaacagctggattactaagtgttttcgtatggccatgtgcctacagcctctgcttccgcga
tgagaaggtcagagat (SEQ ID NO:9)

STAP-2, 98P4B6 SSH fragment

TTTGCACTTTCAGATACCAGACTGAGCTGGAATTGCTCTCTATTGACTCTACTTCTTAAAGCG
GCTGCCCATACATTCCCTCAGCTGTCCCTGCAGTTAGGTGACATGTGACTGAGTGTGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGCTTTTT (SEQ ID NO:10)

A1139607 (testis EST)

aagaaggagaatccatttagcacccctcagcctggctcagtgattcatatgtggcttggaaatacttgggttt
ttctgttgtacttttggaaatcttcttgcacatctgttagcaatgcagtcaactggagagagtccgatttt
ccagtccaaactgggttatttgcacatctgttagcgtttagggcttacatccctgcactgtgtgt
agcccttcaaatttcagatgttgcacatctgttagcgtttagggcttacatccctgcactgtgtgt
tcaagtttgtctaattcatgcgttagacaacacccttacaaggatccgcagggtggaaaggactcaa
acactagaaaaagcattgaatggaaaatcaaattttaaaacaaaggatcaatttagctggaaaaaaaaa (SEQ ID NO:11)

R80991 (placental EST)

ggccgcggcanccgtacgactggctcaacctggcagtcaggcttggccanacaagagccacctctgggtg
aaggaggagggtctggcggtatggagatctacccctccctggagggtctggccctcgccacgttgcctctgt
tgacccactgcccgtccatgtccaaactcgctcaactggagggttcagcttgcgttgcgttgcctctgt
ggccntctgtcgacacactncacacgctcacctacggctggaccgcgcctcgaggagacgcgtacaagtt
tacccctcccccacccatgcacgntcacgctgcgtgtggccctgcgttgcgttgcgttgcgttgcgttgc
tgccttgcattcagccnaga (SEQ ID NO:12)

FIG. 11A

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FIG. 11B

1 15 16 30 31 45 46 60 61 75 76 165 166 180
 MESRKDTNQELWK MKPRNLLEDDYLHK DTGETSMKRPVILH LHOATAHADDEFDCPSE LOHQELPFQOMHLPI KRAATIASLTFYTL 90
 STRAP-1 -----
 STRAP-2 -----
 STRAP-3 -----
 STRAP-4 ----- 0

91 105 106 120 121 135 136 150 151 165 166 180
 LREVTHPLATSHOY FYKIPFLDINNNPDM VSTLQDQVIVPDM PIVYDQANETKXKRSF PIVYDQANETKXKRSF DISPPPAVIAKYSF 180
 STRAP-1 -----
 STRAP-2 ----- D FYKIPFLDINNNPDM VSTLQDQVIVPDM PIVYDQANETKXKRSF PIVYDQANETKXKRSF DISPPPAVIAKYSF 76
 STRAP-3 -----
 STRAP-4 ----- 0

181 195 196 210 211 225 226 240 241 255 256 270
 SYPHAKSMTYCLCNU AYQOQYQONKEADANNE HDVTRMEEYVSIGTY GLAIALAGGDAYTSIPS VPSDLTMRREFPHYTS VPSLYSLDGTSHD 270
 STRAP-1 -----
 STRAP-2 ----- CLPMRDSRPTYFLNN AYQOQYHANTENSNE EFWMRNTEITSPFM SIGLUSLDAVTSIPS VSNALNMRREFSFTOS TIGFVALLLSTSPVQ 166
 STRAP-3 -----
 STRAP-4 ----- -KGENPFT SSAWLSDIVASGI GPFPLVCLGTSIPS VSNAYNMRREFVOS KQGTTLTDCTARY 68
 STRAP-5 ----- -ATWASTW QSSRSMWPXKSHLWVK BEVTRMEEYVSIGTY ALGTSLDAVTSIPS VSNALNMRREFSFTOS SIGFVAYXVLSLTFL 82

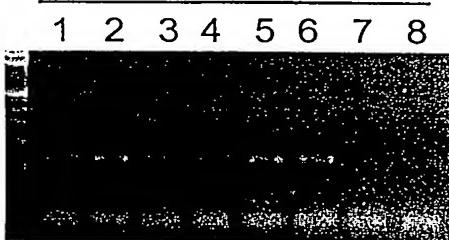
271 285 286 300 301 315 316 330 331 345 346 360
 IFAMNKWDIKOFKW YIPEPTMIAVLPVW VLPKSLIFPCURK KUKLPSICEDVYKI NKTIEICCSOL 339 (SEQ ID NO: 8)
 STRAP-1 -----
 STRAP-2 ----- IYGMRA ----- 173 (SEQ ID NO: 8)
 STRAP-3 ----- VYGRFRFLSLSLNW YLPATAVLGIIPTC PDKIKFVLMIMPCTDN TLTTRDQGTERNSKH ----- 128 (Portion of SEQ ID NO: 8)
 STRAP-4 ----- TYGMRAFFESRYKE YIPEPTMIAVLPVW RSSVAKAIKXLPCTQ P--- ----- 128 (Portion of SEQ ID NO: 8)

~~FIG. 14~~

FIG. 14A

26x

A



B

FIG. 14B

1 2 3 4 5 6 7 8

25x

30x



A

- 1. Brain
- 2. Prostate
- 3. LAPC-4 AD
- 4. LAPC-4 AI
- 5. LAPC-9 AD
- 6. HeLa
- 7. Murine cDNA
- 8. Neg. control

B

- 1. Colon
- 2. Ovary
- 3. Leukocytes
- 4. Prostate
- 5. Small Intestine
- 6. Spleen
- 7. Testis
- 8. Thymus

FIG. 15

FIG. 15A

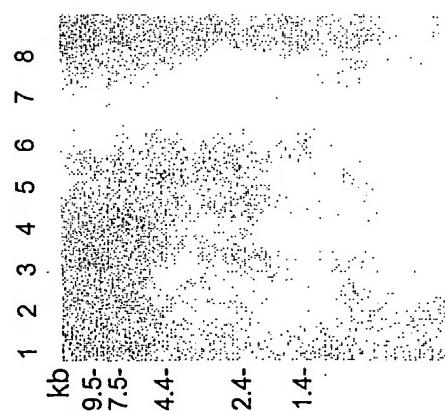


FIG. 15B

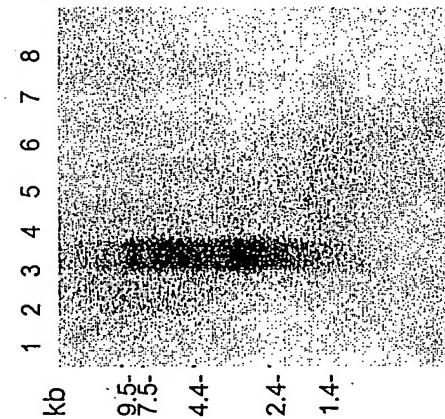
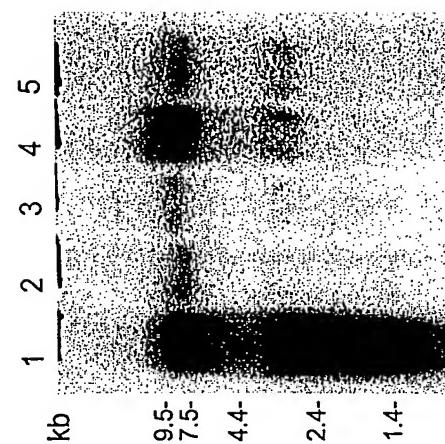


FIG. 15C



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- A
- 1. Heart
 - 2. Brain
 - 3. Placenta
 - 4. Lung
 - 5. Liver
 - 6. Skeletal Muscle
 - 7. Kidney
 - 8. Pancreas

- B
- 1. Spleen
 - 2. Thymus
 - 3. Prostate
 - 4. Testis
 - 5. Ovary
 - 6. Small Intestine
 - 7. Colon
 - 8. Leukocytes

- C
- 1. Prostate
 - 2. LAPC-4 AD
 - 3. LAPC-4 AI
 - 4. LAPC-9 AD
 - 5. LAPC-9 AI

FIG. 17**GDB Comprehei**